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301 TCAAGGACGGTGACTGGAATGAATTCCGTCGTAAACTGACCTTCTATCTGAAAACCTTGG  
-----+-----+-----+-----+-----+-----+ 360  
AGTTCCTGCCACTGACCTTACTTAAGGCAGCATTTGACTGGAAGATAGACTTTTGGAACC

LysAspGlyAspTrpAsnGluPheArgArgLysLeuThrPheTyrLeuLysThrLeuGlu

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361 AGAACGCGCAGGCTCAACAGACCACTCTGTCGCTAGCGATCTTTTAATAAGCTT [SEQ ID NO: 147]  
-----+-----+-----+-----+-----+-----+ 414  
TCTTGCGCGTCCGAGTTGTCTGGTGAGACAGCGATCGCTAGAAAATTATTCGAA [SEQ ID NO: 148]

AsnAlaGlnAlaGlnGlnThrThrLeuSerLeuAlaIlePheEndEnd [SEQ ID NO: 128]